

GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: March 28, 2003, 12:02:57 ; Search time 20.2167 Seconds
(without alignments)
1550.996 Million cell updates/sec

Title: US-09-924-946-2

Perfect score: 4180

Sequence: 1 MAWSPATLFLPFLLLGQPP.....YPANAELSLEQQRUNNLI 756

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4174	99.9	756	1 LOL4 HUMAN	Q96jb6 homo sapien
2	3641.5	87.1	757	1 LOL4_MOUSE	Q924c6 mus musculus
3	2268.5	54.3	774	1 LOL2 HUMAN	Q9y4k0 homo sapien
4	2263	54.1	753	1 LOL3 HUMAN	P58215 mus sapien
5	2222	53.2	754	1 LOL3_MOUSE	Q92175 mus musculus
6	850	20.3	219	1 LOL2_MOUSE	P58022 mus musculus
7	655.5	15.7	1436	1 WC11_BOVIN	P30205 bos taurus
8	633.5	15.2	875	1 NETR_HUMAN	P56730 homo sapien
9	611.5	14.6	761	1 NETR_MOUSE	O08762 mus musculus
10	581	13.9	411	1 LYOX RAT	P16636 rattus norv
11	579	13.9	420	1 LYOX CHICK	Q05063 gallus gall
12	574.5	13.7	411	1 LYOX_MOUSE	P28301 mus musculus
13	572	13.7	417	1 LYOX_HUMAN	P28300 homo sapien
14	561.5	13.4	574	1 LOL1_HUMAN	Q08397 homo sapien
15	483	11.6	532	1 SPER STRPU	P16264 strongyloce
16	461	11.0	347	1 CD5L_HUMAN	O43866 homo sapien
17	445.5	10.7	352	1 CD5L_MOUSE	Q9gwk4 mus musculus
18	374	8.9	668	1 CD6 HUMAN	P30203 homo sapien
19	337.5	8.1	110	1 LOL1_MOUSE	P97873 mus musculus
20	337	8.1	665	1 CD6_MOUSE	Q61003 mus musculus
21	307.5	7.4	458	1 MSRE_MOUSE	P30204 mus musculus
22	303.5	7.3	451	1 MSRE_HUMAN	P21757 homo sapien
23	295.5	7.1	454	1 MSRE_RABIT	Q05585 oryctolagus
24	287.5	6.9	453	1 MSRE_BOVIN	P21758 bos taurus
25	255	6.1	520	1 MRCO_HUMAN	Q9uew3 homo sapien
26	250	6.0	518	1 MTCO_MOUSE	Q60754 mus musculus
27	248.5	5.9	483	1 MRCO_MESAU	Q9wb9 mesocricetu
28	155.5	3.7	1629	1 AT59 HUMAN	Q9p2n4 homo sapien
29	149.5	3.6	495	1 CD5_HUMAN	P06127 homo sapien
30	140	3.3	494	1 CD5_MOUSE	P13379 mus musculus
31	136.5	3.3	491	1 CD5_RAT	P51882 rattus norv
32	123	2.9	583	1 CFAI_HUMAN	P05156 homo sapien
33	122.5	2.9	495	1 CD5_BOVIN	P19238 bos taurus

ALIGNMENTS

RESULT 1

ID	LOL4_HUMAN	STANDARD;	PRT;	756 AA.
AC	Q96JB6; Q96PC0; Q96DY1;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Lysyl oxidase homolog 4 precursor (EC 1.4.3.-) (Lysyl oxidase-like protein 4) (Lysyl oxidase related protein C).			
GN	LOXL4 OR LOXC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_taxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Testis;			
RX	MEDLINE=21316447; PubMed=11292829;			
RA	Ito H., Akiyama H., Iguchi H., Iyama K., Miyamoto M., Ohsawa K., Nakamura T.;			
RT	"Molecular cloning and biological activity of a novel lysyl oxidase-related gene expressed in cartilage.";			
RL	J. Biol. Chem. 276:24023-24029 (2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21550107; PubMed=11691589;			
RA	Maki J.M., Tikkanen H., Kivirikko K.I.;			
RT	Cloning and characterization of a fifth human lysyl oxidase isoenzyme: the third member of the lysyl oxidase-related subfamily with four scavenger receptor cysteine-rich domains.";			
RL	Matrix Biol. 20:493-496 (2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RA	Asuncion L.P., Fogelgren B., Fong K.S.K., Kim Y., Csiszar K.;			
RT	"A novel human lysyl oxidase-like gene (LOXL4) on chromosome 10q24 has an altered SRCR domain and is down-regulated by H-ras.";			
RL	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Eye;			
RA	Straussberg R.;			
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: May modulate the formation of a collagenous extracellular matrix.			
CC	-!- COFACOR: COPPER AND LYSINE TYROSYLQUINONE (LTO) (BY SIMILARITY).			
CC	-!- SUBCELLULAR LOCATION: Extracellular (Potential).			
CC	-!- TISSUE SPECIFICITY: Expressed in many tissues, the highest levels among the tissues studied being in the skeletal muscle, testis and pancreas. Expressed in cartilage.			
CC	-!- PTM: THE LYSINE-TYROSYLQUINONE IS GENERATED BY THE MODIFICATION OF A TYROSYL RESIDUE CROSSLINKED TO THE EPSILON-AMINO GROUP OF A LYSINE (BY SIMILARITY).			
CC	-!- SIMILARITY: CONTAINS 4 SRCR DOMAINS.			
CC	-!- SIMILARITY: BELONGS TO THE LYSYL OXIDASE FAMILY.			

34	120	2.9	1193	1	LMG2_HUMAN	Q13753 homo sapien
35	116	2.8	603	1	CFAI_MOUSE	Q61129 mus musculus
36	113.5	2.7	1877	1	PKCS_MOUSE	Q04592 mus musculus
37	113	2.7	3519	1	OL56_STRAT	Q07017 streptomyce
38	111	2.7	1416	1	YN81_CABEL	Q03610 caenorhabdi
39	110	2.6	2556	1	NTC1_HUMAN	P46531 homo sapien
40	109.5	2.6	1077	1	SM5A_MOUSE	O62217 mus musculus
41	109.5	2.6	2616	1	NDL_DROME	P98159 drosophila
42	109	2.6	867	1	SSPO_BOVIN	P98167 bos taurus
43	107	2.6	1242	1	JAG1_BRARE	Q90y57 brachydanio
44	106	2.5	604	1	CFAI_RAT	Q9uwu3 rattus norv
45	106	2.5	924	1	ICA5_HUMAN	Q9umf0 homo sapien

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DR	EMBL; AF338441; AAK71934.1; -
DR	EMBL; AY036093; AAK64186.1; -
DR	EMBL; AF39536; AAU27543.1; -
DR	EMBL; BC013153; AAH13353.1; -
DR	GeneW; HGNC:17171; LOC14.
DR	InterPro; IPR001695; Lysyl oxidase.
DR	Pfam; PF01186; Lysyl oxidase; 1.
DR	Pfam; PF00530; SRCR_4.
DR	ProDom; PD013887; Lysyl oxidase; 1.
DR	PROSITE; PS00926; LYSYL_OXIDASE; FALSE_NEG.
DR	PROSITE; PS00420; SRCR_1; 1.
DR	PROSITE; PS0287; SRCR_2; 4.
KW	Oxidoreductase; Copper; Glycoprotein; Repeat; Signal.
FT	SIGNAL 1 256 POTENTIAL.
FT	CHAIN 25 756 LYSYL OXIDASE HOMOLOG 4.
FT	DOMAIN 32 133 SRCR 1.
FT	DOMAIN 159 287 SRCR 2.
FT	DOMAIN 311 411 SRCR 3.
FT	DOMAIN 421 529 SRCR 4.
FT	DOMAIN 533 736 LYSYL-OXIDASE LIKE.
FT	METAL 611 611 COPPER (POTENTIAL).
FT	METAL 613 613 COPPER (POTENTIAL).
FT	METAL 615 615 COPPER (POTENTIAL).
FT	MOD_RES 638 638 CROSS-LINKED TO TYROSYLQUINONE (BY SIMILARITY).
FT	MOD_RES 674 674 TYROSYLQUINONE (BY SIMILARITY).
FT	CARBOHYD 198 198 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 629 629 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CONFLICT 3 3 W -> R (IN REF. 4).
FT	CONFLICT 101 101 R -> Q (IN REF. 4).
FT	CONFLICT 405 405 D -> G (IN REF. 3).
FT	CONFLICT 493 493 S -> G (IN REF. 3).
FT	CONFLICT 539 539 A -> T (IN REF. 3).
FT	CONFLICT 542 542 Y -> A (IN REF. 3).
FT	CONFLICT 703 703 Y -> H (IN REF. 3).
SEQ	SEQUENCE 756 AA; 84483 MW; 13051ACADB922BBC CRC64;
Query Match 99.9%; Score 4174; DB 1; Length 756;	
Best Local Similarity 99.9%; Pred. No. 0;	
Matches 755; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1 MAWSPATLFLILLGQPSPPSQLTTLKLVCPSPKEEGLVHLHGQGTVCDD 60
Dd	1 MAWSPATLFLILLGQPSPPSQLTTLKLVCPSPKEEGLVHLHGQGTVCDD 60
Qy	61 NFALQEAIVACROLGFEEAALTWAHSARYQGEGPIWLNVRCVGPTSSLDCCSGNGMGVS 120
Dd	61 NFALQEAIVACROLGFEEAALTWAHSARYQGEGPIWLNVRCVGPTSSLDCCSGNGMGVS 120
Qy	121 DCSHSEDGVVICHPRRHGYLSETVSNALGPQGRLEEVRLKAPILASAKQHSPTVEGAVE 180
Dd	121 DCSHSEDGVVICHPRRHGYLSETVSNALGPQGRLEEVRLKAPILASAKQHSPTVEGAVE 180
Qy	181 VKYEGHWRFQVDCQWTWNNSRVCGMLGPFSEVPVDSSHYYRKVKWLKRDPKSLKSLTN 240
Dd	181 VKYEGHWRFQVDCQWTWNNSRVCGMLGPFSEVPVDSSHYYRKVKWLKRDPKSLKSLTN 240
Qy	241 KNSFWIHQVTCLTGETPHMNCQOVAPARGKLPAFCGGMHAVSCVAGHPFRPEKTKPQ 300
Dd	241 KNSFWIHQVTCLTGETPHMNCQOVAPARGKLPAFCGGMHAVSCVAGHPFRPEKTKPQ 300
Qy	301 RKGSWAEPRVRLRSQAQGEGRVEVLMTNPQTCTCHRNLLISAVYCROLGFGSAREA 360

361	RKGSWAEPERVRURRSGAQVGEGRVEVMNRQWGTCDHRNLLISASVCRQLGFGSAREA	360
361	LFGARLGGGLGPRIHLSEVRRCRGYERTILSDCPALGSGONGCHENAAAVRCNVPMNGFONO	420
361	LFGARLGGGLGPRIHLSEVRRCRGYERTILSDCPALGSGONGQHENDAAVRCNVPMNGFONO	420
421	VRLAGGRIPESGLEVOVENGVNPRMGVSVCSENWGLTEANVACRQLGLGFPAIHAYKETWF	480
421	VRLAGGRIPESGLEVOVENGVNPRMGVSVCSENWGLTEANVACRQLGLGFPAIHAYKETWF	480
481	WSGTPRAEPPVMSVGRSCGTETALQQCORHGPVHCSHGKRFIAGVSCMDSPDLVYNAQ	540
481	WSGTPRAEPPVMSVGRSCGTETALQQCORHGPVHCSHGKRFIAGVSCMDSPDLVYNAQ	540
541	LVQETAYLEDRPLSLQYCAHEENCLSKSAHDMWPYGRI LLRPSTOIYNLGRTDFRPKT	600
541	LVQETAYLEDRPLSLQYCAHEENCLSKSAHDMWPYGRI LLRPSTOIYNLGRTDFRPKT	600
601	GRDSVMWQHCHRHVHSIEVFTHYDLLTLNGSKVAEGHKAFCLEDNTNCPTGLQRRYACAN	660
601	GRDSVMWQHCHRHVHSIEVFTHYDLLTLNGSKVAEGHKAFCLEDNTNCPTGLQRRYACAN	660
661	FGEQGVTGCMWTYRHDIDCQWDITDVGPNYIFQVIIVPHYEVAESDFSNNMLQCRCCK	720
661	FGEQGVTGCMWTYRHDIDCQWDITDVGPNYIFQVIIVPHYEVAESDFSNNMLQCRCCK	720
721	YDGHRVWLHNCHTGNPSYPANAELSLEQEQRLLNNLI	753
721	YDGHRVWLHNCHTGNPSYPANAELSLEQEQRLLNNLI	753

RESULT 2
LOL4_MOUSE STANDARD; PRT; 757 AA.

AC Q924C6;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lysyl oxidase homolog 4 precursor (EC 1.4.3.-) (Lysyl oxidase-like protein 4) (Lysyl oxidase related protein C).
GN LOX14 OR LOXC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP MEDLINE=21316447; PubMed=11292829;
RX Ito H., Akiyama H., Iguchi H., Iiyama K., Miyamoto M., Ohsawa K., Nakamura T.;
RT "Molecular cloning and biological activity of a novel lysyl oxidase-related gene expressed in cartilage."
EL J. Biol. Chem. 276:24023-24029(2001).
CC -!- FUNCTION: May modulate the formation of a collagenous extracellular matrix.
CC -!- COFACTOR: COPPER AND LYSLINE TYROSYLQUINONE (LTQ) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Extracellular (potential).
CC -!- PTM: THE LYSLINE-TYROSYLQUINONE IS GENERATED BY THE MODIFICATION OF A TYROSYL RESIDUE CROSSLINKED TO THE EPILON-AMINO GROUP OF A LYSLINE (BY SIMILARITY).
CC -!- SIMILARITY: CONTAINS 4 SRCR DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE LYSL YL OXIDASE FAMILY.

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CC EMBL; AF338440; AAK71933.1; --
DR MGDI; MG11914823; Lox14.
DR

DR	InterPro; IPR001695; Lysyl oxidase.
DR	InterPro; IPR001190; Srcr receptor.
DR	Pfam; PF01186; Lysyl oxidase; 1.
DR	Pfam; PF00530; SRCR_4.
DR	ProDom; PD013887; Lysyl oxidase; 1.
DR	PROSITE; PS00926; LYSYL_OXIDASE; FALSE_NEG.
DR	PROSITE; PS00420; SRCR_1; 1.
DR	PROSITE; PS00287; SRCR_2; 4.
KW	Oxidoreductase; Copper; Glycoprotein; Repeat; Signal.
FT	SIGNAL 1 25 POTENTIAL.
FT	CHAIN 26 757 LYSYL OXIDASE HOMOLOG 4.
FT	FT DOMAIN 33 134 SRCR 1.
FT	FT DOMAIN 160 288 SRCR 2.
FT	FT DOMAIN 312 412 SRCR 3.
FT	FT DOMAIN 422 530 SRCR 4.
FT	FT DOMAIN 534 737 LYSYL-OXIDASE LIKE.
FT	FT METAL 612 612 COPPER (POTENTIAL).
FT	FT METAL 614 614 COPPER (POTENTIAL).
FT	FT METAL 616 616 COPPER (POTENTIAL).
FT	FT MOD_RES 639 639 CROSS-LINKED TO TYROSYLQUINONE (BY SIMILARITY).
FT	MOD_RES 675 675 TYROSYLQUINONE (BY SIMILARITY).
FT	FT CARBOHYD 199 199 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	FT CARBOHYD 615 615 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	FT CARBOHYD 630 630 N-LINKED (GLCNAC. .) (POTENTIAL).
SEQ	SEQUENCE 757 AA; D9861368F63B7B2A CRC64;
Query Match 87.1%; Score 3641.5; DB 1; Length 757;	
Best Local Similarity 86.4%; Pred No. 8.5e-279;	
Matches 654; Conservative 43; Mismatches 59; Indels 1; Gaps 1;	
QY	1 MAWSPPATLF-F-LULLQQPPSPQSISGTTKLRIVGPESKPGRLEVLHQGMGTVCVD 59
DB	1 MMWPQTTFSLFLLLLSQA PSSRSSGTTKKRLVGPADRPREGRLLEVHLHQGMGTVCVD 60
QY	60 DNFAIQETAVACROLGFPAALTWAHS AKYGQGGEP IWLNDNRCVCTESSLDQCSCNGHCV 119
DB	61 DDFAIQETAVACROLGFESALTWAHS AKYGQGGEP IWLNDNRCVCLGTXTLDCQCSNGMGI 120
QY	120 SDCSHSDVGVIHPRRHRGVLTSETVSNALGPQRRLEEVRKPTLASAKOHS PVTEGAV 179
DB	121 SDCRHSDVGVCVCHPRRQGHGTHSEKVSNALGPQRRLEEVRKPTLASAKHSPVTEGAV 180
QY	180 EVKYEGHWQRVCDQGWTWNNSRVVCGMLGFPSEVPDVSHTYRKVMDLKMDDPKSRKLST 239
DB	181 EVRVDGHWQRVCDQGWTWNNSRVVCGMLGFPSQTSVNSHYRYKVWNLKMKDPKSRNLST 240
QY	240 KNSFWIHHVTCLGTEPHMANCOVOVA PAR KLR PACPGMHAVVSV CVAGPHFRPKTKP 299
DB	241 KNSFWIH RVDCFGTPEPLAKCQVOVAPGRGKLR PACPGMHAVVSV CVAGPHFRPKPKP 300
QY	300 QRKGSWAEP RVLRS GAQGVGEGRVEVLMNRQGWTCVCDHRWNLLSASVVCRQLGPGSARE 359
DB	301 TRKSHAELK VLRLS GAQGVGEGRVEVLMNRQGWTCVCDHRWNLLSASVVCRQLGPGSARE 360
QY	360 ALFGARLCQGLGPIHLSVR CGYERTLSDCPALESGNQGCQHENA AAVRCNVPMNFQN 419
DB	361 ALFGARLCQGLGPIHLSVR CGYERTLGDCLALESGNQGCQHENA AAVRCNI PMMGFN 420
QY	420 QVRLAGGRIP EGGLEVQVEVNGVPRWGSVCSENWGLTEAMVACRQLGLGFALHAYKTW 479
DB	421 KVRLAGGRNS BEGVVEVQVEVNGGPRWGTVCS DHWGLTEAMVTCRQLGLGFANFALKDTW 480
QY	480 FWSGTPRAQEVVMSGVRCSTELAQCCORHGCPVHC SHGGCFLAGVCSMD SAPOLVNNA 539
DB	481 YMQGTPEAKEVVMSSGVRCSTEMALQQCORHGCPVHC SHGGPRFSAGVACMNSAPOLVNNA 540
QY	540 QLVQETAYLEDR PLSQLCAEENCLSKSA DHMDWPYGYRRLLRSTO IYNLRGTRDPRPK 599
DB	541 QLVQETAYLEDR PLSMVLYAEENCLSKSA DHMDWPYGYRRLLRFPSSQ IYNLRADPRPK 600
QY	600 TGDRSWVWHQCHRHYHSIEVFTHYDLLTLINGSKVAEGHKASFCLDETNCPTGLQRRYACA 659

[illegible]

555 QLYCAHEENCLSKADHWDPYGVYRRLLRSTOYINLGRTOPEPKTGRDSWVWVHCHRRHY 614
570 MLCAMEENCLASASAAQDPTTGYVRRLLRSTOYINLGRTOPEPKTGRDSWVWVHCHRRHY 629
615 HSIEVFTHYDLLTLGSKVAEGHKASCFLEDTNCTPTGLQRVACAFNGEQGVTVGMDTY 674
630 HSMEVFTHYDLLNLGSKVAEGHKASCFLEDTNCTPTGLQRVACAFNGEQGVTVGMDTY 689
675 RHDIDCWMDITDVPGNYIFOVIVNPHYVAESDFSNNTLCRCRYDGHVRVLMHNCHTG 734
690 RHDIDCWMDITDVPGNYIFOVIVNPHYVAESDFSNNTLCRCRYDGHVRVLMHNCHTG 749
735 NSYPANAELSLEOEQLRNN 754
750 GSPSEETKPKPEHPSGLLNN 769

RESULT 4
L0L3 HUMAN
ID L0L3 HUMAN STANDARD; PRT: 753 AA.
AC P5915; 056RS1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lysyl oxidase homolog 3 precursor (EC 1.4.3.4) (Lysyl oxidase-like
protein 3).
DE L0L3 OR L0XL,
GN L0L3 OR L0XL,
OS Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
[1] _TaxID=9606;
SEQUENCE FROM N.A.
MEDLINE=21181571; PubMed=11284725;
Waki J.M., Kivirikko K.I.;
"Cloning and characterization of a fourth human lysyl oxidase
isoenzyme";
Biochem. J. 355:381-387(2001).
[2]
SEQUENCE FROM N.A.
MEDLINE=21280915; PubMed=11386757;
Jourdane-Le Saux C., Tomshé A., Uffalusi A., Jia L., Csieszar K.;
"Central nervous system, uterus, heart, and leukocyte expression of
the L0L3 gene, encoding a novel lysyl oxidase-like protein";
Genomics 74:211-218(2001).
[3]
SEQUENCE FROM N.A.
MEDLINE=21233589; PubMed=11334717;
Huang Y., Dai J., Tang R., Zhao W., Zhou Z., Wang W., Ying K., Xie Y.
Mao Y.;
"Cloning and characterization of a human lysyl oxidase-like 3 gene
(L0XL3)";
Matrix Biol. 20:153-157(2001).
-!- COFACTOR: COPPER AND LYSINE TYROSYLLOXINONE (LTO) (BY SIMILARITY)
-!- SUBCELLULAR LOCATION: Extracellular (potential).
-!- TISSUE SPECIFICITY: EXPRESSED IN MANY TISSUES, THE HIGHEST LEVELS
AMONG THE TISSUES STUDIED BEING SEEN IN THE PLACENTA, HEART,
OVARY, TESTIS, SMALL INTESTINE AND SPLEIN.
-!- PM: THE LYSINE-TYROSYLLOXINONE IS GENERATED BY THE MODIFICATION
OF A TYROSYL RESIDUE COVALENTLY LINKED TO THE EPISILON-AMINO GROUP OF A
LYSINE (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 4 SRCR DOMAINS.
-!- SIMILARITY: BELONGS TO THE LYSYL OXIDASE FAMILY.

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DR EMBL: AF282619; AAK51671.1; --
 DR EMBL: AF311313; AAK63205.1; --
 DR EMBL: AF284815; AAK91134.1; --
 DR GenBank: HGNC:13869; LoxL3.
 DR InterPro: IPR001695; Lysyl oxidase.
 DR InterPro: IPR001190; Srcr_receptor.
 DR Pfam: PF00530; SRCR; 4.
 DR Pfam: PF01186; Lysyl oxidase; 1.
 DR PRINTS: PRO0074; LYSILOXIDASE.
 DR PRINTS: PRO0258; SPERACTRCPTR.
 DR ProDom: PD013887; Lysyl oxidase; 1.
 DR SMART: SM00202; SR; 4.
 DR PROSITE: PS00926; LYSYL_OXIDASE; 1.
 DR PROSITE: PS00420; SRCR_1; 1.
 DR PROSITE: PS0287; SRCR_2; 4.
 KW Oxidoreductase; Copper; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 753 LYSYL OXIDASE HOMOLOG 3.
 FT DOMAIN 44 145 SRCR 1.
 FT DOMAIN 169 282 SRCR 2.
 FT DOMAIN 307 407 SRCR 3.
 FT DOMAIN 417 525 SRCR 4.
 FT DOMAIN 529 732 LYSYL-OXIDASE LIKE.
 FT METAL 607 607 COPPER (POTENTIAL).
 FT METAL 609 609 COPPER (POTENTIAL).
 FT METAL 611 611 COPPER (POTENTIAL).
 FT MOD_RES 634 634 CROSS-LINKED TO TYROSYLQUINONE (BY SIMILARITY).
 FT MOD_RES 670 670 TYROSYLQUINONE (BY SIMILARITY).
 FT CARBOHYD 111 111 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 266 266 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 481 481 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 625 625 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 159 159 E -> K (IN REF. 3).
 SQ SEQUENCE 753 AA; 83166 MW; 582C46DA25E05A69 CRC64;

Query Match 54.1%; Score 2263; DB 1; Length 753;
 Best Local Similarity 54.1%; Pred. No. 2.5e-170;
 Matches 419; Conservative 105; Mismatches 205; Indels 40; Gaps 10;

QY 3 WSPATLFL--LIGOPPS-----RPOSLLTTLRLVGPSPKSGEGLVHLGQWG 55
 DB 9 WSPGULLLCLSCSLGSPSPSTGPEKAGSQG-LRFLAGFPKRYEGREIQRAGWG 67
 QY 56 TVCDNFAICEATVACROLGFEAALTAHSAKYQGEPTWLDNVRVCGTFESSLDGSGN 115
 DB 68 TICDDFTLQAAILCRELFTTATGTHSAKYGPGTGRIWLDNLSGSGTEQSVTECASR 127
 QY 116 GWGVSDCHSDGVICHPRRHRYGLSETYSNALGPQRRLEEVRLKPYLASAKQHSPTV 175
 DB 128 GWGNSDCTHEDAGVICKQQLRFGSDSNVIEV--EHLQVVEVRIRPAVGMGRRPLPVT 185
 QY 176 EGAVEVYGEHQRVQCDQGMNNSRVVCMGLGFPSEVPVDSHYKRWDLKMRDPKSL 235
 DB 186 EGLVELRLPCWQVQCDKGMASHNVSHVCMGLGFPSEKRYNAAFY-----RL 232
 QY 236 KSLTNKNSFWIHOVTCLGTEPHMANQOVAPARGKLRPACPGGMHVVSCVAGPHF--- 292
 DB 233 LAORQQHSFGLHGACVGTGAHLSLCSLEFYRANDTAR--CPGGFAVWSCVPGPVYAS 290
 QY 293 ----RPPKTPQRKGSMAEPRVRLRSGAQVGRVEVLNMRQWGTCDHRMNLISASVV 348
 DB 291 SGQKQKQSQKQ-----GEARVRLKGAHPGGRVEVLKASTGTGVCWKDLHAASVV 344
 QY 349 CRLQFGSAREALFGARLGGGLGPIHLSEVRRCGYERTLSDCPALGSGQNGCHENAAV 408
 DB 345 CRELQFGSAREALSGARMQGMGAHLSEVRSCQQLSLWKCPKNTATBDCSHSQDAGV 404
 QY 409 RCNVPNMGFQNVRLAGRIPEGLLEVOVEVNGVPRWGSVCSENKGLTEAMVACQLGL 468
 DB 405 RCNLPYTGAETIRLSGSRSGHEGRVEVGTGGPGLRWGLIGICDDWGTLEAMVACQLGL 464

QY 469 GFATHAYKETWFSGTTPRAQEVVMVGVRCSGTETALQOCQHPG-VHCSHGGGRFLAGVS 527
 DB 465 GYANHGLQETWYWD-SGNITEVVMVGVRCTGTSLDQCAHHGTHITCKRTGTFTAGVI 523
 QY 528 CWDGAPDLVMAQLVQETAYLSDPLSOLYCAHEENCLSKSADHMDWPGYVRRLLRFSQ 587
 DB 524 CSETASDLLHLSALVQETAYIEDRPLMLYCAEENCLASSARSANWPGYHRRLLRFSQ 583
 QY 588 IYNLGRDTFRPKTGRDSVMWHQCHRHYSIEVFTHYDLTLTLNGSKVAGHKASFCLEDTN 647
 DB 584 IHNLGRADFRPKAGRHSSWWHECHGHVHSMDFTHYDILTNGTKVAGHKASFCLEDTN 643
 QY 648 CPTGLQRYACANFGEQGVTCWDYRHDIDCQWDTIDVPGNYIFQVIVNPHYFAE 707
 DB 644 CQEDSVSKYECANFGEQGITVGCWDLRHDIDCQWDTIDVPGNYILQVIVNPHYFAE 703
 QY 708 SDFSNNMLQCRCKYDGHVWLNHCHTNGSYPANAELSLEQORLRNLI 756
 DB 704 SDFTNAMCKCKYDGHRIWVHCHIGDAFSEANRRFRYPGQTSNQI 752

RESULT 5
 LOL3 MOUSE STANDARD; PRT; 754 AA.
 AC Q9Z175; Q9UJ39;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lysyl oxidase homolog 3 precursor (EC 1.4.3.-) (Lysyl oxidase-like protein 3) (Lysyl oxidase related protein 2).
 DE LoxL3 OR LOR2.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_taxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAINS=C57BL/6J, and 129/SvJ; TISSUE=Muscle;
 RX MEDLINE=99126643; PubMed=9927484;
 RA Jang W., Hua A., Spilson S.V., Miller W., Roe B.A., Meisler M.H.;
 RT "Comparative sequence of human and mouse BAC clones from the mnd2 region of chromosome 2p13.";
 RL Genome Res. 9:53-61(1999).
 CC -!- COFACTOR: COPPER AND LYSINE TYROSYLQUINONE (LTQ) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Extracellular (Potential).
 CC -!- PTM: THE LYSINE-TYROSYLQUINONE IS GENERATED BY THE MODIFICATION OF A TYROSYL RESIDUE CROSSLINKED TO THE EPSILON-AMINO GROUP OF A LYSINE (BY SIMILARITY).
 CC -!- SIMILARITY: CONTAINS 4 SRCR DOMAINS.
 CC -!- SIMILARITY: BELONGS TO THE LYSYL OXIDASE FAMILY.
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 CC EMBL: AF053368; AAC83205.1; --
 DR EMBL: AF084363; AAC95338.1; --
 DR MGD: MGI:1337004; LoxL3.
 DR InterPro: IPR001695; Lysyl oxidase.
 DR InterPro: IPR001190; Srcr_receptor.
 DR Pfam: PF00530; SRCR; 4.
 DR Pfam: PF01186; Lysyl oxidase; 1.
 DR PRINTS: PRO0074; LYSILOXIDASE.
 DR PRINTS: PRO0258; SPERACTRCPTR.
 DR ProDom: PD013887; Lysyl oxidase; 1.
 DR SMART: SM00202; SR; 4.
 DR PROSITE: PS00926; LYSYL_OXIDASE; 1.
 DR PROSITE: PS00420; SRCR_1; 1.
 DR PROSITE: PS0287; SRCR_2; 4.

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KW Oxidoreductase; Copper; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 754
 FT DOMAIN 45 146
 FT DOMAIN 170 283
 FT DOMAIN 308 408
 FT DOMAIN 418 526
 FT DOMAIN 530 733
 FT DOMAIN 608 608
 FT METAL 610 610
 FT METAL 612 612
 FT MOD_RES 635 635
 FT MOD_RES 671 671
 FT CARBOHYD 112 112
 FT CARBOHYD 267 267
 FT CARBOHYD 391 391
 FT CARBOHYD 482 482
 FT CARBOHYD 626 626
 FT CARBOHYD 754 754
 SQ SEQUENCE 754 AA; 83681 MW; 87584009434FAFF2 CRC64;

Query Match 53.2%; Score 2222; DB 1; Length 754;
 Best Local Similarity 54.0%; Pred. No. 4.2e-167;
 Matches 413; Conservative 111; Mismatches 195; Indels 46; Gaps 11;

Qy 13 LLLL-----GPPPP--SRPOS LGT--TKLPLVGPESKPEGRLEVLHQGWGTICDD 60
 Db 14 LLLHLCLCSFSGVSPSISPEKKVGGQGRFLRAGFPKPYEGVEIQRAGEMGTICDD 73
 Qy 61 NFAIQEATVACRQLGFAALTAHSAKYGGEGPIWLDNVRCVGTSTSSLDQCSNGWGS 120
 Db 74 DFTLQAAHVLCRELGFTATGWTHTSAKYGGTGRWLDNLSCRGTEGVTVCASRWGNS 133
 Qy 121 DCSHSDGVTCHEPRRHYGLSEVSNALPOGR-RLEEVRLKPILASAKQHSPTTEGAV 179
 Db 134 DCTHDEDAGVICKDQRLGP---SDSNVIEHQVQVEVRLPAVEMGRRLPVTTEGLV 190
 Qy 180 EYKYGHRVQVDCQWNTWNNRSRVGCMGPSPVDSHYVRYKVDLKMDRPKSLKSLT 239
 Db 191 EVRLPEGMSOVCDKQWNSAHNSHVGCMGPGPEKRVNWFYRLAOKK-----238
 Qy 240 NKNSEWIIHOVTCLTGTEPHMANCQVQVAPARGKLRPACPGMHVAVVSCVAGPHF-----292
 Db 239 -QHSFGLHSVACVGTAEHLSCLEFFRYANDTTR--CSGGNPVAVSVGLGLVATFTGQK 295
 Qy 293 RPPKTKPQKGSWAEPRVRLPSGAQVCGEGRVEVLNMQVCTCDHRWNLSASVWCRL 352
 Db 296 KQOHSKPO-----GEARVRLKGAHQEGEGRVEVLKAGTGTCTGCDKWDLQAASVWCPEL 349
 Qy 353 GFGSAREALFGARLGGGLPIHLSEVRCBGYERTLSDCPALEGSGQNGCOHENAAVRCNV 412
 Db 350 GFGTAREALSGARMGQGMGAHLSEVRCBGQPSLWRCPSKNITAECDHSHQDAGVRCNL 409
 Qy 413 PNMFGQVQLRACGRIPPEGLLEQVQVNGVPRWGSVCSENWGLTEAMVACRQLGLGPAI 472
 Db 410 PYTGVEVKIPLSGRSRYEGREVEQVIGIPGHLRWGLICGDDMGTLTEAMVACRQLGLGVAN 469
 Qy 473 HAYKETHFWSCGTFRADQVNVMSVGRCSGTETALQOCORHGP-VHCSHGGRGLAGVSCMDS 531
 Db 470 HGLQETWYWD-SGNVTEVMSVGRCTGSELSLNOCAHHSSHITCKTKGTGRTAGVICSET 528
 Qy 532 APDLVMAQLVQETAYLEDPLSOLYCAHEENCLSKSADHMDPYPGYRLLRFSTQIYNL 591
 Db 529 ASDLLLSALVQETAYITEDPLHMLYCAAEENCLASASAKNPYGHRLRLRFSSQIHNL 588
 Qy 592 GRTDFPKTGRDSVWVHCQHRHYSIEVFTHYDILLTNGSKVAEGHKAFCLEDTNCTG 651
 Db 589 GRADFRPKAGRHSVWVHCCHYHSMDFIHYDILTPNGTKVAEGHKAFCLEDTNCTG 648
 Qy 652 LQRYACANFCEQVTVGCWDTYRHDIDCQWVDITDVGPNYIFQVIVNPHYVEAESDPS 711
 Db 649 VSKRYECANFCEQGITVGCWDLYRHDIDCQWIDITDVKPGNYILQVIVNPHYVEAESDFT 708

Qy 712 NNMLQCRCKYDGHVWLHNCHTGNSYPANAELEQEOBLNNLJ 756
 Db 709 NNAMKCKYDGHRIWVHNCIHGDAPSEANRRFRYPGQTSNQI 753

RESULT 6

ID LOL2 MOUSE STANDARD; PRT; 219 AA.
 AC P58022; Q9JJ39;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lysyl oxidase homolog 2 (EC 1.4.3.-) (Lysyl oxidase-like protein 2)
 DE (Fragment).
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20303100; PubMed=10842102;
 RA Tourdan-Le Saux C., Le Saux O., Gleyzal C., Sommer P., Csizsar K.;
 RT "The mouse lysyl oxidase-like 2 gene (mLOXL2) maps to chromosome 14
 and is highly expressed in skin, lung and thymus.";
 RL Matrix Biol. 19:179-183(2000).
 CC -1- COPACTOR: COPPER AND LYSINE TYROSYLQUINONE (LTO) (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Extracellular (Potential).
 CC -1- TISSUE SPECIFICITY: UBIQUITOUS. HIGHEST EXPRESSION IN SKIN, LUNG
 CC AND THYMUS.
 CC -1- PTM: THE LYSINE-TYROSYLQUINONE IS GENERATED BY THE MODIFICATION OF
 CC A TYROSYL RESIDUE CROSSLINKED TO THE EPSILON-AMINO GROUP OF A
 CC LYSINE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE LYSYL OXIDASE FAMILY.
 CC
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 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL; AF117951; AAF29046.1; -;
 CC MGD; MGI:2137913; Lox12.
 CC InterPro; IPR001695; Lysyl oxidase.
 CC Pfam; PF01186; Lysyl oxidase; 1.
 CC PRINTS; PR00074; LYSYLOXIDASE.
 CC PRODOM; PD013887; Lysyl oxidase; 1.
 CC PROSITE; PS00926; LYSYL_OXIDASE; 1.
 CC Oxidoreductase; Copper; Glycoprotein.
 KW NON TER 1 1 LYSYL-OXIDASE LIKE.
 FT DOMAIN <1 196 COPPER (POTENTIAL).
 FT METAL 71 71 COPPER (POTENTIAL).
 FT METAL 73 73 COPPER (POTENTIAL).
 FT METAL 75 75 COPPER (POTENTIAL).
 FT MOD_RES 98 98 CROSS-LINKED TO TYROSYLQUINONE (BY
 FT SIMILARITY).
 FT MOD_RES 134 134 TYROSYLQUINONE (BY SIMILARITY).
 FT CARBOHYD 89 89 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 219 AA; 25564 MW; 7FAC4DB4A98P2144 CRC64;

Query Match 20.3%; Score 850; DB 1; Length 219;
 Best Local Similarity 66.5%; Pred. No. 8.3e-60;
 Matches 141; Conservative 34; Mismatches 37; Indels 0; Gaps 0;

Qy 543 QETAYLEDPLSOLYCAHEENCLSKSADHMDPYPGYRLLRFSTQIYNLGRTPPKTGR 602
 Db 3 EQTAYLEDPLSOLYCAHEENCLSKSADHMDPYPGYRLLRFSTQIYNLGRTPPKTGR 62
 Qy 603 DSWVWVHCQHRHYSIEVFTHYDILLTNGSKVAEGHKAFCLEDTNCTGLORRVACANFG 662
 Db 63 HAWIWHDCRHHYSMEVFTHYDILLTNGSKVAEGHKAFCLEDTNCTGLORRVACANFG 122

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RESULT 8
NETR HUMAN
ID NETR HUMAN STANDARD; PRT; 875 AA.
AC P56730; Q9U16;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neurotropsin precursor (EC 3.4.21.-) (Motopsin) (Leydin).
PRSS12.
GN PRSS12.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98201705; PubMed=9540828;
RA Proba K., Gschwend T.P., Sonderegger P.;
RT Cloning and sequencing of the cDNA encoding human neurotropsin.;
RL Biochim. Biophys. Acta 1396:143-147(1998).
RN [2]
RP SEQUENCE OF 615-875 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=99203523; PubMed=10103056;
RA Poorafshar M., Heilman L.;
RT Cloning and structural analysis of leydin, a novel human serine
protease expressed by the Leydig cells of the testis.;
RL Eur. J. Biochem. 261:244-250(1999).
CC -!- ACTION: PLAYS A ROLE IN NEURONAL PLASTICITY AND THE PROTEOLYTIC
ACTION MAY SUBSERVE STRUCTURAL REORGANIZATIONS ASSOCIATED WITH
LEARNING AND MEMORY OPERATIONS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted
CC -!- TISSUE SPECIFICITY: Brain and Leydig cells of the testis.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
CC -!- SIMILARITY: CONTAINS 4 SRCR DOMAINS.
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
CC EMBL; AJ001531; CAA04816.1; -
CC EMBL; AF077298; AAD25919.1; -
CC HSP; P00763; IDPO.
CC Genew; HGNC:9477; PRSS12.
CC MIM; 606709; -
CC MEROPS; S01.217; -
CC Interpro; IPR001314; Chymotrypsin.
CC Interpro; IPR000001; Kringle.
CC Interpro; IPR001254; Ser_protease_Try.
CC Interpro; IPR001190; Ser_receptor.
CC Pfam; PF00051; kringle; 1.
CC Pfam; PF00089; trypsin; 1.
CC Pfam; PF00530; SRCR; 4.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PRINTS; PR00258; SPERACTRCPT.
CC ProDom; PD000395; kringle; 1.
CC SMART; SM00130; KR; 1.
CC SMART; SM00202; SR; 4.
CC SMART; SM00020; Tryp_SPC; 1.
CC PROSITE; PS00021; KRINGLE1; FALSE_NEG.
CC PROSITE; PS50070; KRINGLE2; 1.
CC PROSITE; PS50420; SRCR_1; 3.
CC PROSITE; PS50287; SRCR_2; 4.
CC PROSITE; PS50240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC Hydrolase; Serine protease; Glycoprotein; Kringle; Repeat; Signal.
KW

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FT SIGNAL 1 20
FT CHAIN 21 875
FT DOMAIN 93 165
FT DOMAIN 170 271
FT DOMAIN 280 381
FT DOMAIN 387 487
FT DOMAIN 500 601
FT DOMAIN 619 875
FT DOMAIN 619 875
FT ACT_SITE 630 631
FT ACT_SITE 726 726
FT ACT_SITE 825 825
FT DISULFID 619 750
FT CARBOHYD 26 26
FT CARBOHYD 683 683
FT CONFLICT 701 701
FT CONFLICT 839 841
FT CONFLICT 875 875
FT SEQUENCE 875 AA; 97011 MW; B66EC946DC2081C8 CRC64;

Query Match 15.2%; Score 633.5; DI.1; Length 875;
Best Local Similarity 31.4%; Pred. No. 4.9e-42;
Matches 159; Conservative 54; Mismatches 69; Indels 125; Gaps 15;

QY 32 LRLVGPESKPEGRLEVLHOGQWTVCDNFAIQEATVA;RQLGFEA-ALTWASAKYGO 90
Db 280 IRLAG-GSSVHGVRVLYHAGQWTVCDNFAIQEATVA;RQLGFEA-ALTWASAKYGO 90
QY 91 GEGFIMLDNVRVCGTSSLDQCSNGWVSDCSHSDVG/IHPRRHGYLSETVSNALG 150
Db 338 GSGFVMDLDEVRCTGNELSIQCFKSSWGHNCHKEDAG/SCTP-----LTDGVIRIAG 391
QY 151 PQGRRLBEVLKPIASAKOHSPVTEGAVEVKEGHWQ/CDQWMTMNSRVVCCMLGFP 210
Db 392 GKGS-----EGRLVYRGWGT/CDQWMTMNSRVVCCMLGFP 431
QY 211 SEVPVDSHYRYKVDLMKMRDPKSLTNKNSFWIHQVTCGLGTEPHMANCOVOVAFRG 270
Db 432 YGKQASANFEE-----STGPIWLDVDSGSGKTRFLQCS-----RRQ 469
QY 271 KLRPACFGMHAVVSCVAGPHFPPTKPKQKGSMAEEFR-----VLRPSAQVGEGRV 324
Db 470 WGRHDCSHREDVSIACYPG-----GEGHRLSLGFPVRLMDGHNKKEGRV 513
QY 325 EVLMNRQWGTVCDEHWNLIASVVCRLGFGSAREALFCARLCQGLGPIHLSEVRCRGYE 384
Db 514 EVFINGQWGTTCDDGWTDKRAVICRQLGYKGPARTWYAFCEGKGPVHVDNVCKTGNE 573
QY 385 RTLSDCPALEGSONGCOHENAAAVRCNVPMNGFQNVRIAGRIPEEGLELVEQVNGVP 444
Db 574 RSLADCIKQDIGHNCRHSEDAGVICDY--FG-----KTAGSNKESL-----615
QY 445 RWGVSVCSENWGLTEAMVACRLGFGFAIHAYKETWFS(TPRAQEVVMGVRCSGTAL 504
Db 616 ---SSVC---GL--RLHRRQKRIIGGKNSLRGGMPQVSLRLKS-----652
QY 505 QQCQRHGPVHCHGGGRFLAGVSCMDS 531
Db 653 -----SHGDGRLLCGATILSS 668

RESULT 9
NETR MOUSE
ID NETR MOUSE STANDARD; PRT; 761 AA.
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neurotropsin precursor (EC 3.4.21.-) (Motopsin) (Brain-specific serine
protease 3) (BSSP-3).
GN PRSS12 OR BSSP3.

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OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97401523; PubMed=9245503;
 RA Gschwend T.P., Krueger S.R., Kozlov S.V., Wolfer D.P., Sonderegger P.;
 FT "Neurotrophin, a novel multidomain serine protease expressed in the
 RT nervous system";
 RL Mol. Cell. Neurosci. 9:207-219(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98008948; PubMed=9344839;
 RA Yamamura Y., Yamashiro K., Tsuruoka N., Nakazato H., Tsujimura A.,
 RA Yamaguchi N.;
 RT "Molecular cloning of a novel brain-specific serine protease with a
 RT kringle-like structure and three scavenger receptor cysteine-rich
 RT motifs";
 RL Biochem. Biophys. Res. Commun. 239:386-392(1997).
 CC -!- FUNCTION: PLAYS A ROLE IN NEURONAL PLASTICITY AND THE PROTEOLYTIC
 CC ACTION MAY SUBSERVE STRUCTURAL REORGANIZATIONS ASSOCIATED WITH
 CC LEARNING AND MEMORY OPERATIONS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: MOST ABUNDANT IN CEREBRAL CORTEX, HIPPOCAMPUS
 CC AND AMYGDALA.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 3 SRCR DOMAINS.
 CC
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 CC
 DR EMBL: Y13192; CAA73646.1; -;
 DR EMBL: D89871; BAA23986.1; -;
 DR HSSP: P00763; LDPO.
 DR MEROPS: S01.237; -;
 DR MGD: MGI:1100881; Prrs12.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR001190; Src_receptor.
 DR Pfam: PF00051; kringle; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR Pfam: PF00530; SRCR; 3.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRINGLE; FALSE_NEG.
 DR PRINTS: PR00256; SPERACTRCPTR.
 DR ProDom: PD000395; Kringle; 1.
 DR SMART: SM00130; KR; 1.
 DR SMART: SM00202; SR; 3.
 DR SMART: SM00020; Tryp_SPC; 1.
 DR PROSITE: PS00021; KRINGLE_1; FALSE_NEG.
 DR PROSITE: PS00070; KRINGLE_2; 1.
 DR PROSITE: PS00420; SRCR_1; 3.
 DR PROSITE: PS00287; SRCR_2; 3.
 DR PROSITE: PS02440; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Serine protease; Glycoprotein; Kringle; Repeat; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 761 NEUROTROPYPSIN.
 FT DOMAIN 85 157 KRINGLE.
 FT DOMAIN 166 267 SRCR 1.
 FT DOMAIN 273 373 SRCR 2.
 FT DOMAIN 386 487 SRCR 3.
 FT DOMAIN 505 761 SERINE PROTEASE.

FT	DOMAIN	505	516	ZYMOGEN ACTIVATION REGION.
FT	ACT_SITE	516	517	REACTIVE BOND (POTENTIAL).
FT	ACT_SITE	562	562	CHARGE RELAY SYSTEM.
FT	ACT_SITE	612	612	CHARGE RELAY SYSTEM.
FT	ACT_SITE	711	711	CHARGE RELAY SYSTEM.
FT	DISULFID	505	636	POTENTIAL.
FT	CARBOHYD	93	93	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	521	521	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	569	569	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	761 AA;	84118 MW;	DP507B03712164B6 CRC64;

Query Match 14.6%; Score 611.5; DB 1; Length 761;
 Best Local Similarity 29.3%; Pred. No. 2.2e-40;
 Matches 165; Conservative 57; Mismatches 184; Indels 157; Gaps 17;

QY	4	SPPTATLFLFLLLGQP	-----PPSRP	-----QSLGTTKRLVLG	36
Db	114	SPPAS---	WAEALRGOPHNFCHSPDGSGRPCWCFYRNAQGVKDWGVCDCGQGPALPVLVLG	170	
QY	37	PESKPEGRLEVLHGGQWGTVCDDNFAIQEATVACRQLGFEA-ALTMASAKYGGEGPI	95		
Db	171	GNS-GHEGRVELYHAGWGTICDDQNDNADADVICRQLGLSLGIKAW-HQAHFGEESGPI	228		
QY	96	WLDNVRVCGTSSLDCCGNGWGVSDCSHSDVGVICHPRHRGVLSETVSNALGPQRR	155		
Db	229	LLDEVRCVTGNELSIQCPKSWGHNCHGKEDAGVSCVP	282		
QY	156	LEEVRKLKILASAKQHSPTVEGAVEYEGHWRQVCDQGTGMMNSRVVCGMLGFPSEVPV	215		
Db	293	-----EGRLEVVYKGGWGTVCDDGWTMTYVACRLLGFK	317		
QY	216	DSHYRKVMDLKMHPKSLTNKNSFWIHQVTCLEPHMANCQVQVAPARGKLPA	275		
Db	318	---YKGQSSVNHFDGSRN-----PILLDDVSCSGKEVSFTQCS	360		
QY	276	CPGGMHVVVCV-----AGHPRPPTKTPQKGSWAEPRVLRSAQVGEGRVEVLM	328		
Db	361	CSHREDVGLTCTPYDSDGHLSPGF	403		
QY	329	NROWGTVCDRHWNLTASVVCVCRQLGFGSAREALFGARLQGLPIHLSEVRCRGVETLS	388		
Db	404	NGQWGTICDDGWTDKHAAVICRQLGKGPARTWAYFEGKGPIMNDVKTGNEKALA	463		
QY	389	DCPALEGSQNGQHENAARVCRNPNMGFQNVRLAGGRIPLEGLELVQVEVNGVPRMGS	448		
Db	464	CCVKQDIGHNCRHSEDAGVICD	499		
QY	449	VCSENVGLTEAMVACRQLGLGFAIHAYKETWFSGTTPRAQEVWVGVCSTELALQCCQ	508		
Db	500	MLSSGCGL--RLHRRQRKRIIGNNSLRGAWPQASLR	535		
QY	509	RHGPVHCSHGGRFLAGVSCMDS	531		
Db	536	----LRSAGDGRLLCGATLLSS	554		

RESULT 10
 LYOX RAT
 ID LYOX RAT STANDARD; PRT; 411 AA.
 AC P16636;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein-lysine 6-oxidase precursor (EC 1.4.3.13) (Lysyl oxidase).
 GN LOX.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Aorta;
 RX MEDLINE=90304121; PubMed=1973052;

Wed Apr 2 09:14:01 2003

RA Trackman P.C., Pratt A.M., Wolanski A., Tang S.-S., Offner G.D.,
 RA Troxler R.F., Kagan H.M.;
 RT "Cloning of rat aorta lysyl oxidase cDNA: complete codons and
 RT predicted amino acid sequence";
 RL Biochemistry 29:4863-4870(1990).
 RN [2]

RP REVISIONS.
 RX MEDLINE=91329411; PubMed=1678281;
 RA Trackman P.C., Pratt A.M., Wolanski A., Tang S.-S., Offner G.D.,
 RA Troxler R.F., Kagan H.M.;
 RT "Cloning of rat aorta lysyl oxidase cDNA: complete codons and
 RT predicted amino acid sequence";
 RL Biochemistry 30:8282-8282(1991).
 CC -!- FUNCTION: IT IS RESPONSIBLE FOR THE POSTTRANSLATIONAL OXIDATIVE
 CC DEMINATION OF PEPTIDYL LYSINE RESIDUES IN PRECURSORS TO FIBROUS
 CC COLLAGEN AND ELASTIN.
 CC -!- CATALYTIC ACTIVITY: Peptidyl-L-lysyl-peptide + H(2)O + O(2) =
 CC peptidyl-allysyl-peptide + NH(3) + H(2)O(2).
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- TISSUE SPECIFICITY: AORTA AND LUNG.
 CC -!- PTM: THE LYSINE-TYROSYLQUINONE IS GENERATED BY THE MODIFICATION OF A
 CC A TYROSYL RESIDUE CROSSLINKED TO THE EPSILON-AMINO GROUP OF A
 CC LYSINE (BY SIMILARITY).
 CC -!- PTM: The N-terminus is blocked.
 CC -!- SIMILARITY: BELONGS TO THE LYSYL OXIDASE FAMILY.

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CC EMBL; U11038; AAC52176.1; -;
 CC EMBL; J02903; AAA41537.1; -;
 CC PIR; A30352; A30352; Lysyl oxidase.
 CC Pfam; PF01186; Lysyl oxidase; 1.
 CC PRINTS; PR00074; LYSYLOXIDASE.
 CC ProDom; PD013887; Lysyl oxidase; 1.
 CC PROSITE; PS00926; LYSYL OXIDASE; 1.
 CC Oxidoreductase; Copper; Signal; Glycoprotein.
 CC SIGNAL 1 21
 CC PROPEP 22 264
 CC CHAIN 765 411
 CC DOMAIN 207 411
 CC METAL 286 286
 CC METAL 288 288
 CC METAL 290 290
 CC METAL 314 314
 CC MCD_RES 314 314
 CC CROSS-LINKED TO TYROSYLQUINONE (BY
 CC SIMILARITY).
 CC TYROSYLQUINONE (BY SIMILARITY).
 CC N-LINKED (GLCNAC...) (POTENTIAL).
 CC N-LINKED (GLCNAC...) (POTENTIAL).
 CC SEQUENCE 411 AA; 46558 MW; EE68C9C5AACDFCLIA CRC64;
 Query Match 13.9%; Score 581; DB 1; Length 411;
 Best Local Similarity 49.8%; Pred. No. 2.6e-38;
 Matches 112; Conservative 32; Mismatches 69; Indels 12; Gaps 5;

QY 509 RHGVPHVCHSGGRLAGVSCMSAPDLVMAQLVQETAYLEDRPLSOLYCAHEENCLSKS 568
 Db 192 RHRP--GYGTGYFOYGL-----PDLVPDPYVIAQSTYVQKMSYMLNRCAAEEENCLCLASS 242
 QY 569 ADHWD-WPYGYRLLRSTQIYNLGRDTRPKTGDSWVWHQCHRRHYSIEVFTYDILLT 627
 Db 243 AYRADVDRDYDRHVLRLFPQRKNGTSDFLPSRPRYSWEHWSCHQHYHSMDFSHYDILLD 302
 QY 628 LNGS-KVAEGHKGAFCLDNTCPCTGLQRRYACANFGQVTVGCNDRYHDDCOMVDIT 686
 Db 303 ASTQRRVAEGHKGAFCLDNTCPCTGLQRRYACANFGQVTVGCNDRYHDDCOMVDIT 361

QY 687 DVQPGNVIFQVIVNPHYVEAESDFSNMLQCRCKYDGHVRVLHNC 731
 Db 362 DVQPGNVILKVSUNPSYLVPSDYSNNVRCREIRYTGHHHA'ASGC 406

RESULT 11

LYOX CHICK STANDARD; PRT; 420 AA.
 ID Q05063;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein-lysine 6-oxidase precursor (EC 1.4.3.13) (Lysyl oxidase).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN (1) _TaxID=9031;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA MEDLINE=93077497; PubMed=1360009;
 RX Wu Y., Rich C.B., Lincecum J., Trackman P.C., Kagan H.M., Foster J.A.;
 RT "Characterization and developmental expression of chick aortic lysyl
 RT oxidase";
 RL J. Biol. Chem. 267:24199-24206(1992).
 CC -!- FUNCTION: IT IS RESPONSIBLE FOR THE POSTTRANSLATIONAL OXIDATIVE
 CC DEMINATION OF PEPTIDYL LYSINE RESIDUES IN PRECURSORS TO FIBROUS
 CC COLLAGEN AND ELASTIN.
 CC -!- FUNCTION: IN ADDITION TO CROSS LINKING OF EXTRACELLULAR MATRIX
 CC PROTEINS IT MAY HAVE A DIRECT ROLE IN TUMOR SUPPRESSION.
 CC -!- CATALYTIC ACTIVITY: Peptidyl-L-lysyl-peptide + H(2)O + O(2) =
 CC peptidyl-allysyl-peptide + NH(3) + H(2)O(2).
 CC -!- COFACTOR: COPPER AND LYSINE TYROSYLQUINONE (LTO) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- DEVELOPMENTAL STAGE: INCREASES BETWEEN DAY 8 AND 16 OF EMBRYONIC
 CC DEVELOPMENT, DURING AORTIC EMBRYOGENESIS, IN DIRECT PROPORTION
 CC TO TOTAL PROTEIN SYNTHESIS.
 CC -!- PTM: THE LYSINE-TYROSYLQUINONE IS GENERATED BY THE MODIFICATION OF A
 CC A TYROSYL RESIDUE CROSSLINKED TO THE EPSILON-AMINO GROUP OF A
 CC LYSINE (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE LYSYL OXIDASE FAMILY.
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 CC or send an email to license@isb-sib.ch).

CC EMBL; M97881; AAA48942.1; -;
 CC PIR; A45166; A45166;
 CC InterPro; IPR001695; Lysyl oxidase.
 CC Pfam; PF01186; Lysyl oxidase; 1.
 CC PRINTS; PR00074; LYSYLOXIDASE.
 CC ProDom; PD013887; Lysyl oxidase; 1.
 CC PROSITE; PS00926; LYSYL OXIDASE; 1.
 CC Oxidoreductase; Copper; Signal; Glycoprotein.
 CC SIGNAL 1 21
 CC PROPEP 22 153
 CC CHAIN 154 420
 CC DOMAIN 216 420
 CC DOMAIN 58 286
 CC METAL 295 295
 CC METAL 297 297
 CC METAL 299 299
 CC METAL 323 323
 CC MCD_RES 323 323
 CC CROSS-LINKED TO TYROSYLQUINONE (BY
 CC SIMILARITY).
 CC TYROSYLQUINONE (BY SIMILARITY).
 CC N-LINKED (GLCNAC...) (POTENTIAL).
 CC SEQUENCE 420 AA; 48152 MW; E0CBEB1DD621F5C2 CRC64;

Query Match 13.9%; Score 579; DB 1; Length 420;
 Best Local Similarity 49.8%; Pred. No. 3.9e-38;
 Matches 114; Conservative 31; Mismatches 72; Indels 12; Gaps 5;

QY 505 QOCORHGVCHSGGREFLAGVSCMSAPDLVWNAQLVQETAYLEDRPLSOLYCAHEENC 564
 Db 197 RQSRVRP---GVTGYFQVGL-----PDLVPDPYIQASTYVQKMSYNLRCAAEENC 247
 QY 565 LKSAADHMD-WPYGYRLLRFSTQIYNLGRDTPRPKTGRDSWWHCHRRHYSIEVFTHY 623
 Db 248 LASSAYRADVRDYNRLRFPQVRKNQGTSDFLPSRPRYSWEMHSCQHYHSMDEFSHY 307
 QY 624 DLLTLNG-SKVAEGHKASFCLEDTNCTGLQRRYACANFGEQGVTCWDTYRHIDICQW 682
 Db 308 DLLDASSHRKVAEGHKASFCLEDTSCDYGYYRYACTAH-TQGLSPGCDYTNADIDCQW 366
 QY 683 VDJTVDGPGNYIFQVTVNPHYVAESDFSNMLOCRCKYDGHVRWLHNC 731
 Db 367 IDITDKPGNYILKVSVPESDYNNIVRCDIRYTGHHAYASGC 415

RESULT 12
 LYOX_MOUSE
 ID LYOX_MOUSE STANDARD; PRT; 411 AA.
 AC P28301;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein-lysine 6-oxidase precursor (EC 1.4.3.13) (Lysyl oxidase)
 DE (RAS excision protein).
 GN LOX OR RRG.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91343916; PubMed=1678898;
 RA Kenyon K., Contente S., Trackman P.C., Tang J., Kagan H.M.,
 RA Friedman R.M.;
 RT "Lysyl oxidase and rrg messenger RNA";
 RL Science 253:802-802(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=NIH Swiss;
 RX MEDLINE=93300513; PubMed=8100214;
 RA Contente S., Csizsar K., Kenyon K., Friedman R.M.;
 RL "Structure of the mouse lysyl oxidase gene";
 RL Genomics 16:395-400(1993).
 CC -!- FUNCTION: IT IS RESPONSIBLE FOR THE POSTTRANSLATIONAL OXIDATIVE
 CC DEMINATION OF PEPTIDYL LYSINE RESIDUES IN PRECURSORS TO FIBROUS
 CC COLLAGEN AND ELASTIN
 CC -!- FUNCTION: REGULATOR OF RAS EXPRESSION. MAY PLAY A ROLE IN TUMOR
 CC SUPPRESSION.
 CC -!- CATALYTIC ACTIVITY: Peptidyl-L-lysyl-peptide + H(2)O + O(2) =
 CC peptidyl-allysyl-peptide + NH(3) + H(2)O(2).
 CC -!- COFACTOR: COPPER AND LYSINE TYROSYLQUINONE (LTO) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- PTM: THE LYSINE-TYROSYLQUINONE IS GENERATED BY THE MODIFICATION OF
 CC A TYROSYL RESIDUE CROSSLINKED TO THE EPSILON-AMINO GROUP OF A
 CC LYSINE (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE LYSYL OXIDASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; M65142; AAA19032.1; -.

DR EMBL; M65143; AAA20185.1; -.
 DR EMBL; L04262; AAA99899.1; -.
 DR EMBL; L04263; AAA99899.1; JOINED.
 DR EMBL; L04264; AAA99899.1; JOINED.
 DR MGD; MGI:96817; Lox.
 DR InterPro: IPR001695; Lysyl oxidase.
 DR Pfam: PF01186; Lysyl oxidase; 1.
 DR PRINTS; PR00074; LYSYLOXIDASE.
 DR PRODOM; PD013887; lysyl oxidase; 1.
 DR PROSITE; PS00926; LYSYL OXIDASE; 1.
 KW Oxidoreductase; Copper; Signal; Glycoprotein.
 FT SIGNAL 1 21 POTENTIAL.
 FT PROPEP 22 264 POTENTIAL.
 FT CHAIN 765 411 PROTEIN-LYSINE 6-OXIDASE.
 FT DOMAIN 207 411 LYSYL-OXIDASE LIKE.
 FT METAL 286 286 COPPER (POTENTIAL).
 FT METAL 288 288 COPPER (POTENTIAL).
 FT METAL 290 290 COPPER (POTENTIAL).
 FT MOD_RES 314 314 CROSS-LINKED TO TYROSYLQUINONE (BY
 FT SIMILARITY).
 FT MOD_RES 349 349 TYROSYLQUINONE (BY SIMILARITY).
 FT CARBOHYD 91 91 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 138 138 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 333 333 A -> G (IN REF. 2).
 SQ SEQUENCE 411 AA; 46700 MW; DBC0563A9C0AEB52 CRC64;

Query Match 13.7%; Score 574.5; DB 1; Length 411;
 Best Local Similarity 50.2%; Pred. No. 8.5e-38;
 Matches 109; Conservative 32; Mismatches 67; Indels 9; Gaps 4;

QY 517 HGGGRFLAGVSCMSAPDLVWNAQLVQETAYLEDRPLSOLYCAHEENC LKSAADHMD-WP 575
 Db 197 YGTGYFQVGL-----PDLVPDPYIQASTYVQKMSYNLRCAAEENC LASSAYRADVRD 250
 QY 576 YGYRELLRFSTQIYNLGRDTPRPKTGRDSWWHCHRRHYSIEVFTHYDLLTLNGS-KVA 634
 Db 251 YDHRVLLRFPQVRKNQGTSDFLPSRPRYSWEMHSCQHYHSMDEFSHYDLLDANTQKVA 310
 QY 635 EGHKASFCLEDTNCTGLQRRYACANFGEQGVTCWDTYRHIDICQWVDITDVGPGNYI 694
 Db 311 EGHKASFCLEDTSCDYGYYRYACTAH-TQGLSPGCDYTAADIDCQWIDITDVGPGNYI 369
 QY 695 FQVIVNPHYVAESDFSNMLOCRCKYDGHVRWLHNC 731
 Db 370 LKVSVPESDYNNIVRCDIRYTGHHAYASGC 406

RESULT 13
 LYOX_HUMAN
 ID LYOX_HUMAN STANDARD; PRT; 417 AA.
 AC P28300;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Protein-lysine 6-oxidase precursor (EC 1.4.3.13) (Lysyl oxidase).
 GN Lox.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=93024096; PubMed=1357535;
 RA Mariani T.J., Trackman P.C., Kagan H.M., Eddy R.L., Shows T.B.,
 RA Boyd C.D., Deak S.B.;
 RT "The complete derived amino acid sequence of human lysyl oxidase and
 RT assignment of the gene to chromosome 5 (extensive sequence homology
 RT with the murine ras recision gene).";
 RL Matrix 12:242-248(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92128932; PubMed=1685472;

RA Haemaelaeninen E.R., Jones T.A., Sheer D., Taskinen K.,
 RA Pihlajaniemi T., Kivirikko K.I.,
 RT "Molecular cloning of human lysyl oxidase and assignment of the gene
 RT to chromosome 5q23.3-31.2.",
 RL Genomics 11:508-516(1991).
 RN [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=9318011; PubMed=10391127;
 RA Contente S., Kenyon K., Sriman P., Subramanyan S., Friedman R.M.;
 RA "Epigenetic inhibition of lysyl oxidase transcription after
 RT transformation by ras oncogene";
 RL Mol. Cell. Biochem. 194:79-91(1999).
 RN [4]
 RN SEQUENCE OF 55-216 FROM N.A.
 RP TISSUE=Blood;
 RC MEDLINE=92332554; PubMed=1352776;
 RX Svinarich D.M., Twomey T.A., Macauley S.P., Krebs C.J., Yang T.P.,
 RA Krawetz S.A.;
 RT "Characterization of the human lysyl oxidase gene locus";
 RL J. Biol. Chem. 267:14382-14387(1992).
 RN [5]
 RN DISEASE.
 RP PubMed=9111998;
 RX Khakoo A., Thomas R., Trompeter R., Duffy P., Price R., Pope F.M.;
 RA "Congenital cutis laxa and lysyl oxidase deficiency";
 RL Clin. Genet. 51:109-114(1997).
 RN [6]
 RN VARIANT GLN-158.
 RX MEDLINE=93300514; PubMed=8100215;
 RA Csaszar K., Mariani T.J., Gosin J.S., Deak S.B., Boyd C.D.;
 RT "A restriction fragment length polymorphism results in a
 RT nonconservative amino acid substitution encoded within the first exon
 RT of the human lysyl oxidase gene";
 RL Genomics 16:401-406(1993).
 CC -!- FUNCTION: RESPONSIBLE FOR THE POSTTRANSLATIONAL OXIDATIVE
 CC DEAMINATION OF PEPTIDYL LYSINE RESIDUES IN PRECURSORS TO FIBROUS
 CC COLLAGEN AND ELASTIN. IN ADDITION TO CROSS-LINKING OF
 CC EXTRACELLULAR MATRIX PROTEINS, MAY HAVE A DIRECT ROLE IN TUMOR
 CC SUPPRESSION.
 CC -!- CATALYTIC ACTIVITY: Peptidyl-L-lysyl-peptide + H(2)O + O(2) =
 CC peptidyl-allysyl-peptide + NH(3) + H(2)O(2).
 CC -!- COFACTOR: COPPER AND LYSYL TYROSYLQUINONE (LTQ).
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- PTM: THE LYSYL-TYROSYLQUINONE IS GENERATED BY THE MODIFICATION OF A
 CC A TYROSYL RESIDUE CROSS-LINKED TO THE EPSILON-AMINO GROUP OF A
 CC LYSINE.
 CC -!- DISEASE: Deficiency in lysyl oxidase has been found in patients
 CC with autosomal recessive cutis laxa.
 CC -!- SIMILARITY: BELONGS TO THE LYSYL OXIDASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; M94054; AAA59525.1; -;
 CC EMBL; S45875; AAB23549.1; -;
 CC EMBL; S78694; AAB21243.1; -;
 CC EMBL; AF039291; AAD02130.1; -;
 CC EMBL; M84150; AAA59541.1; -;
 CC PIR; S23515; S23515.
 CC PIR; A40557; A40557.
 CC Genew; HGNC:6664; LOX.
 CC MIM; 153455; -;
 CC InterPro; IPR001695; Lysyl oxidase.
 CC Pfam; PF01186; Lysyl oxidase; 1.
 CC PRINTS; PF00074; LYSYLOXIDASE.
 CC PRODOM; PD013887; Lysyl oxidase; 1.
 CC PROSITE; PS00926; LYSYL_OXIDASE; 1.
 CC Oxidoreductase; Copper; Signal; Glycoprotein; Polymorphism.
 KW

FT SIGNAL 1 21
 FT PROPEP 22 270
 FT CHAIN 271 417
 FT DOMAIN 213 417
 FT METAL 292 292
 FT METAL 294 294
 FT METAL 296 296
 FT MOD_RES 320 320
 FT MOD_RES 355 355
 FT CARBOHYD 81 81
 FT CARBOHYD 97 97
 FT CARBOHYD 144 144
 FT VARIANT 158 158
 FT CONFLICT 102 102
 FT CONFLICT 137 137
 FT CONFLICT 139 139
 FT CONFLICT 304 305
 FT CONFLICT 315 315
 FT SEQUENCE 417 AA; 46944 MW; 6412A78443E03:04 CRC64;
 SQ
 Query Match 13.7%; Score 572; DB 1; Length 417;
 Best Local Similarity 48.9%; Pred. No. 1.4e-37;
 Matches 110; Conservative 34; Mismatches 69; Indels 12; Gaps 5;
 QY 509 RHGVHCHSGGRFLAGVSCMSAPDLVMAQIVQETAYLEDRPLSOLYCAHEENCLSKS 568
 Db 198 RYRP--GYGTGYFQVGL-----PDLVADPPYIQASTVQKSMYNLRCAAEENCLAST 248
 QY 569 ADHMD-WPGYRRLRPFSTQIYNLGRTPFRPTGRDSWVWVHCHRHYSIEVTHYDLIT 627
 Db 249 AYRADVDYDHRVLLRPPQVKVQGTSDFLPSPRYSMWHSCHQHYHSMDFSHYDLID 308
 QY 628 LNSG-KVAEGHKASPCLEDTNCTGLQRRYACANFGEQCVTVGCNDTYRHIDDCQWVDIT 686
 Db 309 ANTORRAEAGHKASPCLEDTSCDYGVRHFACTAH-TQLSPGCVDTYGADIDCOWIDIT 767
 QY 687 DVGRNVIQVIVNPHYVEAESDFSNMLQCRCKYDGHVNLHNC 731
 Db 368 DVKPGNVIKVSVPNSVLPESDYTNVVRCDIRYTGHIAYASGC 412
 RESULT 14
 LOU1 HUMAN
 ID LOU1 HUMAN STANDARD; PRT; 574 AA
 AC Q08397; Q96BW7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lysyl oxidase homolog 1 precursor (EC 1.4.3.-) (lysyl oxidase-like
 DE protein 1) (LOL).
 DE LOX1L OR LOXL.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin fibroblast;
 RX MEDLINE=93366738; PubMed=7689553;
 RA Kenyon K., Modi W.S., Contente S., Friedman R.M.;
 RT "A novel human cDNA with a predicted protein similar to lysyl oxidase
 RT maps to chromosome 15q24-q25";
 RL J. Biol. Chem. 268:18435-18437(1993).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Placenta;
 RC Kenyon K., Sathya G., Contente S., Friedman R.M.;
 RA "Structure of the human lysyl oxidase-like gene";
 RL Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.

```

RC TISSUE=Lung;
RA Submitted R.;
RL Submitter (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -!- COFACTOR: COPPER AND LYSINE TYROSYLQUINONE (LTO) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Extracellular (Potential).
CC -!- PTM: THE LYSINE-TYROSYLQUINONE IS GENERATED BY THE MODIFICATION OF
CC A TYROSYL RESIDUE CROSSLINKED TO THE EPSILON-AMINO GROUP OF A
CC LYSINE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LYSYL OXIDASE FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; L21186; AAA50162.1; -.
DR EMBL; U24389; AAA68940.1; -.
DR EMBL; U24395; AAA68940.1; JOINED.
DR EMBL; U24394; AAA68940.1; JOINED.
DR EMBL; U24393; AAA68940.1; JOINED.
DR EMBL; U24391; AAA68940.1; JOINED.
DR EMBL; U24390; AAA68940.1; JOINED.
DR EMBL; BC015090; AAH15090.1; -.
DR GenBank; HGNC:6665; LoxL1.
DR MIM; 153456; -.
DR InterPro; IP0001695; Lysyl oxidase.
DR Pfam; PF01186; Lysyl oxidase; 1.
DR PRINTS; PRO0074; LYSYLOXIDASE.
DR ProDom; PD013887; Lysyl oxidase; 1.
DR PROSITE; PS00926; LYSYL OXIDASE; 1.
KW Oxidoreductase; Copper; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT PROPEP 26 94 POTENTIAL.
FT CHAIN 95 574 LYSYL OXIDASE HOMOLOG 1.
FT DOMAIN 370 574 LYSYL-OXIDASE LIKE.
FT DOMAIN 261 267 POLY-PRO.
FT METAL 449 449 COPPER (POTENTIAL).
FT METAL 451 451 COPPER (POTENTIAL).
FT METAL 453 453 COPPER (POTENTIAL).
FT MOD_RES 477 477 CROSS-LINKED TO TYROSYLQUINONE (BY
FT SIMILARITY).
FT MOD_RES 512 512 TYROSYLQUINONE (BY SIMILARITY).
FT CONFLICT 141 141 L -> R (IN REF. 3).
FT SEQUENCE 574 AA; 63066 MW; EE550D4FF2C8ED48 CRC64;
Query Match 13.4%; Score 561.5; DB 1; Length 574;
Best Local Similarity 46.9%; Pred. No. 1.4e-36;
Matches 122; Conservative 28; Mismatches 87; Indels 23; Gaps 6;
QY 483 GTPRAQVWVSGVRCST-----ELALQOCORHPVHCHGGGRFLAGVSCWDSAPDL 535
DB 322 GPRALEPPVLPVRSSDTPPPGGERNAQQGRSLVSGVSRPNQNGRGL-----PDL 372
QY 536 VMAAQLVQETAYLEDRPLSOLYCAHENCLSKSA--DHMDWPGYGRLLRFFSTQYINLG 592
DB 373 VPDENVQASTYVQRAHLYSLRCAEKCLASTAYAPEATD--YDRVLLRFFQVRVNOG 430
QY 593 RTDFRPKTRGDSWWHQCHRHYSIEVFTHYDLL-TINGSKVAGHKASFCLEDTNCPTG 651
DB 431 TADFLLPNRPHRTWEHSCQHYHSMDFSHYDLDATGKKAEGHKASFCLEDTSCDFG 490
QY 652 LQRYACANFGEQVTVGCWDTYRHDIDCQWDLTDVPGNYI;FOVINPHYEVASDFS 711
DB 491 NLKRYACTSH--TQGLSPGCVDTYNADIDCQWIDITDVPQGNILKRVNPKYLVLESDF 549
QY 712 NNMLQCRCKYDGHVWHLNC 731
DB 550 NNVRNCNIHTGRVVSATNC 569

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RESULT 15
SPER_STRPU STANDARD; PRT; 532 AA.
AC P16264;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Egg peptide speract receptor precursor.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Echinozoa; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
OX NCBI_TaxID=7668;
[1]
SEQUENCE FROM N.A., AND SEQUENCE OF 477-489.
RX MEDLINE=89184581; PubMed=2538832;
RA Dangott L.J., Jordan J.E., Bellet R.A., Garbers D.L.;
RT "Cloning of the mRNA for the protein that crosslinks to the egg
RT peptide speract.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:2128-2132(1989).
CC -!- FUNCTION: RECEPTOR FOR THE EGG PEPTIDE SPERACT.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 4 SRCR DOMAINS.
CC
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CC
DR EMBL; J04518; AAA30078.1; -.
DR PIR; A32751; A32751.
DR InterPro; IP001190; Srcr_receptor.
DR Pfam; PF00530; SRCR 4.
DR PRINTS; PRO0258; SPERACTRCPT.
DR SMART; SM00202; SR; 4.
DR PROSITE; PS00420; SRCR 1; 4.
DR PROSITE; PS0287; SRCR 2; 4.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 30
FT CHAIN 31 532 EGG PEPTIDE SPERACT RECEPTOR.
FT DOMAIN 31 491 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 492 520 POTENTIAL.
FT DOMAIN 521 532 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 43 144 SRCR 1.
FT DOMAIN 153 257 SRCR 2.
FT DOMAIN 264 366 SRCR 3.
FT DOMAIN 382 485 SRCR 4.
FT CARBOHYD 78 78 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 532 AA; 57820 MW; 742533E09576CB8 CRC64;
Query Match 11.6%; Score 483; DB 1; Length 532;
Best Local Similarity 27.7%; Pred. No. 1.8e-30;
Matches 149; Conservative 66; Mismatches 216; Indels 106; Gaps 19;
QY 32 LRLVGPEKPEGRLEVLHQGWGTVDNFAIQEATVACRQGFALTAHSAKYGG 91
DB 43 IRLIHGRTE-NEGSEVIYHATRWGGVCDWWHMANVNTCKQGFGARQFYRAYFGAH 101
QY 92 EGFILNDVRCVGTSSLDQSGNGMGVS-DCSHSEDDGVICHPRRHRGYSLETYSNALG 150
DB 102 VTFVYKNNCLGNRELDCCYHRFPLWLCNAOWAAGVECLPKDE----- 148
QY 151 POGRRLEEVRLKPIIASAKQHSPTVEGAVEVKEGHWQVCDQGTMMNSRVVCGMLGFP 210
DB 149 POG-----SLRMILGDVP-----NEGTLTFWCGAWGSVCHTDFGPDGNVACQMGVS 197
QY 211 ---SEVPVDSHYRKVMDLKMDDPKSLTKNSFWIHQVTCLGTEPHMANCOVQVAP 267

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Db 198 RGKSIKTDGHFG-----FSTGPILLDAVDCGTEAHITECHNMPVTP 239
QY 268 ARGKLRPACPGMHAHVSVVAGPHFRPPKTPORKGSWAEPRVRLRSQAQVGEGRVEVL 327
Db 240 -----YQHACFYTHNDVGVVCKENV-----EGDIRLMDGSGPHEGRVEIW 280
QY 328 MNRQWGTVCDBRWNLLISASVVCRLGFGSAREA--LFGARLGGGLGPIHLSEVRCRGYER 385
Db 281 HDDAWGTICDDGMDWADANVVCRAQYRGAVKASGFGEFGFTWAPIHTSFVMTCTGVED 340
QY 386 TLDSCPALGSGONGCOHENAARVC-----NVPNMGFQNOVRLAGRIPEEGLLEVOVE 439
Db 341 RLIDCILRDGWTSHSVHVEDASVVCATDDDDTIEIEPKHTRIVG-----MGQGGCRVE 395
QY 440 VNGVPRWGSVCSENWGLTEAMVACRLGLGFAIHAYKETWFMMSGTPRAQEV-----490
Db 396 VSLGNGWGRVCDPDWSDHEAKTVCYHAG-----YK--WGASRAAGSAEVSAPFDLEAP 446
QY 491 -VMSGVRCSGTE-LALQOCOR--HGFVHCSHGGGRFLAGVSCMDS-APDLVMAQLV 542
Db 447 FIIDGITCSGVENETLSQCMKVSADMTCATGD-----VGVVCEGSTAPESGMSIAVI 499

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Job time : 25.2167 secs